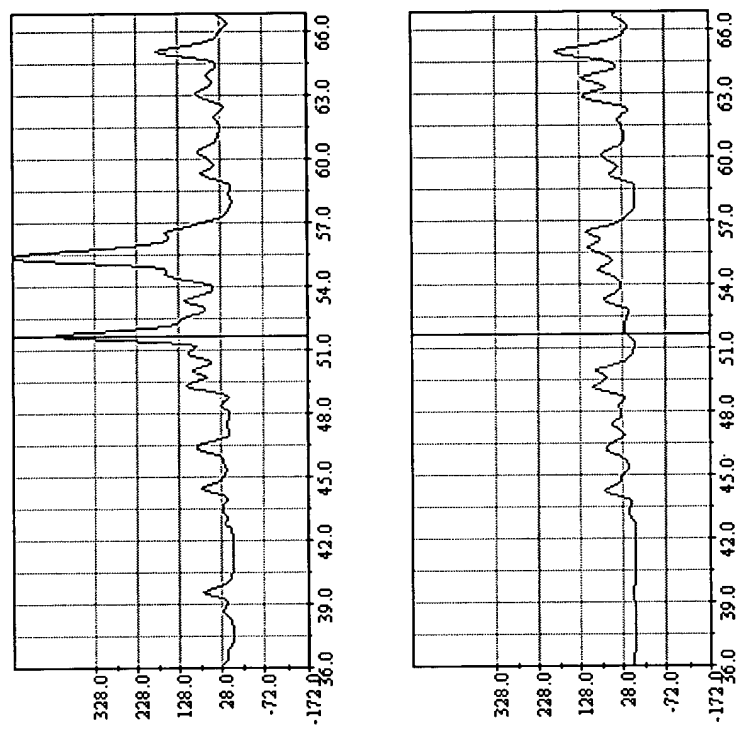


[illegible]

Sequence

; GAP of: W0h051-7.Seq check: 6926 from: 1 to: 52

seq of dicamba induced band w0c0 51.7

to: Cjlp181r.Seq check: 2737 from: 1 to: 714

Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Nwsgapdna.Cmp
CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	520	Length:	714
Ratio:	10.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	5
.	=	1

W0h051-7.Seq x Cjlp181r.Seq..

1gctagctgcgccgtgaccacgacat	26
1	CGATCGAAGTGGTGTGTCAGCTAGCTAGCTGCGCCGTGACCAACGCACAT	50
27	gaccgcagtgcgcgctgatca.....	52
51	GACCGCAGTGC GCGGGGCTGATCAAGGAAAGTATCGGATGGAGCTG	100

Figure 2

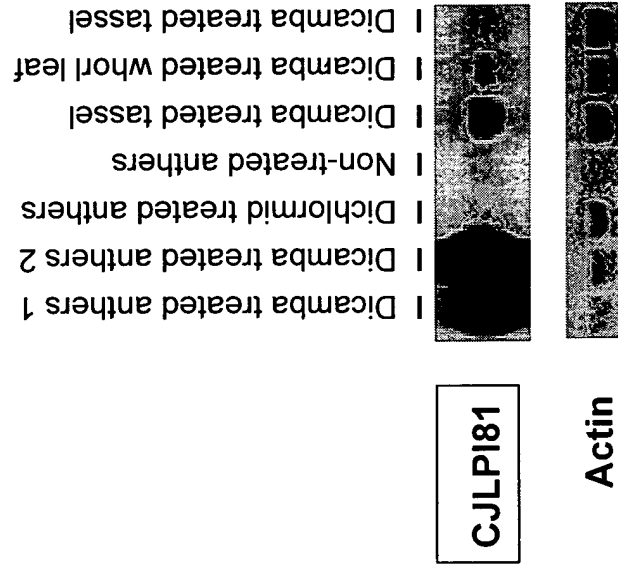


Figure 3

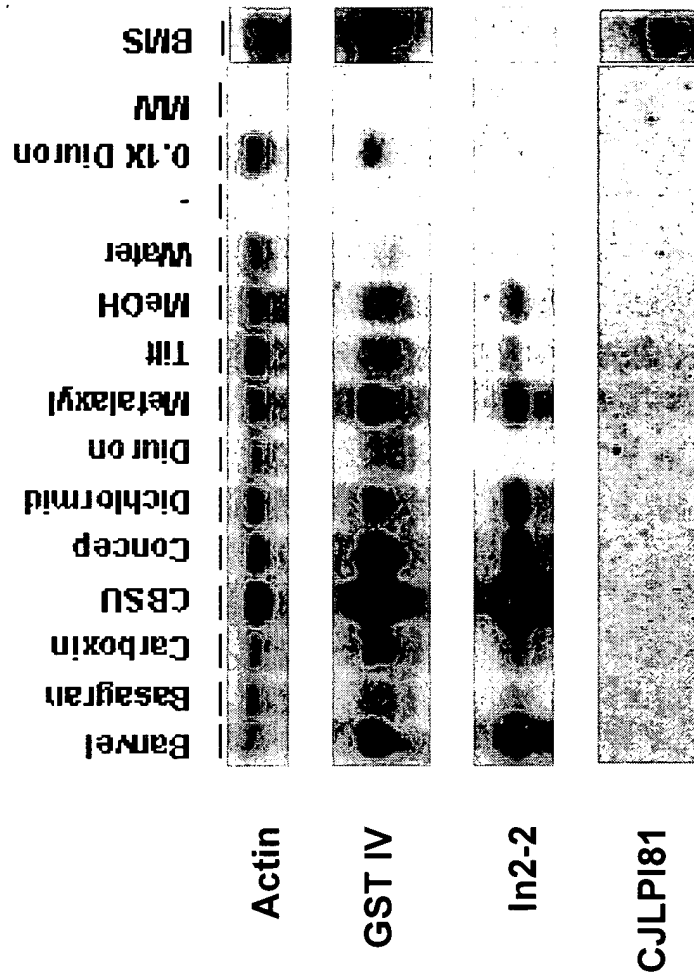


Figure 4

[illegible]

ZmAxi gl 1 MELELGLAPPNP HQPLAAAAEFVGLSSAGSCGNKRVLGDAFGAAKAAT 50

PS-IAA4/5 1 mefkate lrl gl.pg.....iteeeekiihgssvvnknkr..... 36

DOMAIN I NLS

51 LPLFVCEDGDGGGDRDRDGVVDHEQQSNNVPRKKRLVGWPPVKARRRS 100

35 qlpqtseesvsiskvtndehi.vesssaappakaki vgwppirsyrkns 84

101CGGGYVKVKLEGVPIGRKVDVSIHGSYOELLRTLESMPGSGNQD 145

85 lheadvgg ifvkvsmdgapylrkidlrvyggy sellkaletmfkl.tige 133

β α

146 HAEDEVVSHERRRRHPYVVTYEDGEDWLLVGDDVPWEVFKSVKRLKI 195

134 yseregykgse.....yaptyedkdgdwmlvg.dvpwdmfvtscrlri 176

196 LA..... 197

177 mkgteakglgcgv 189

Figure 5

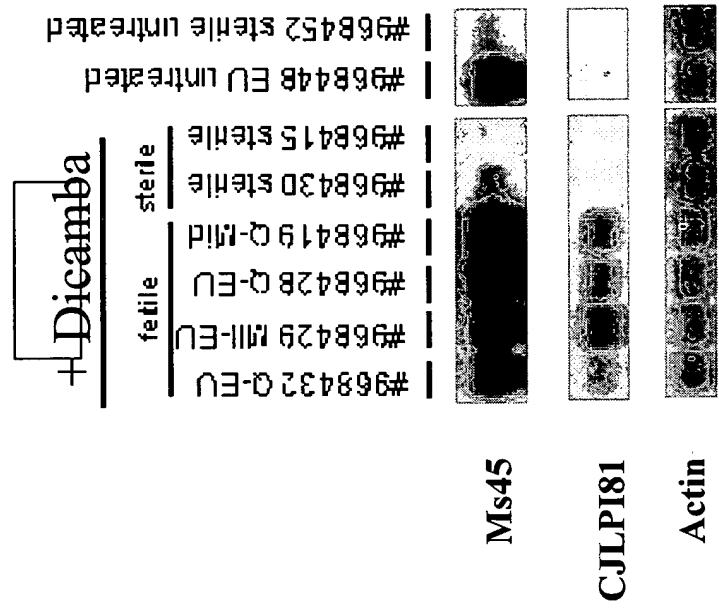


Figure 6

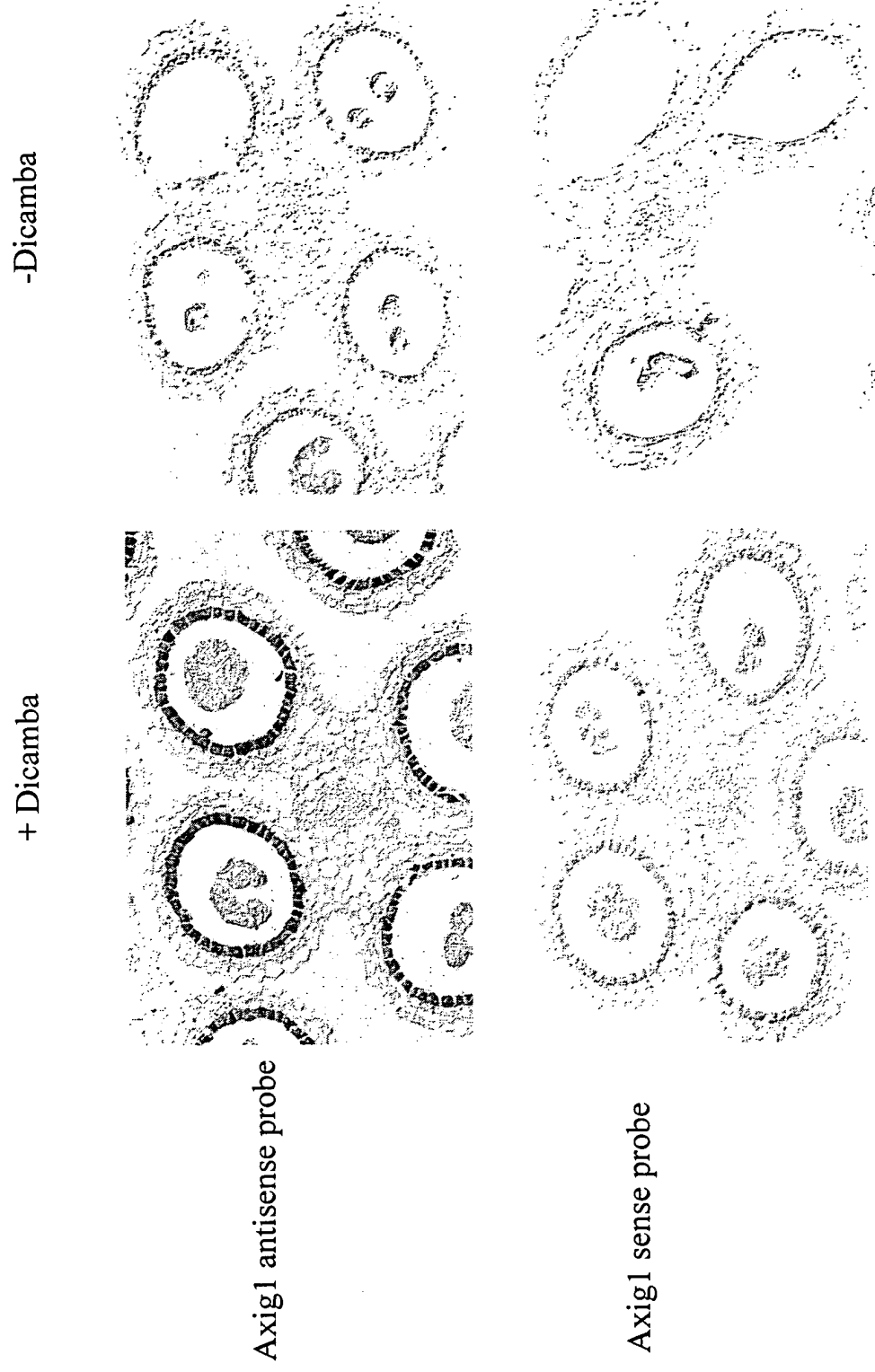


Figure 7

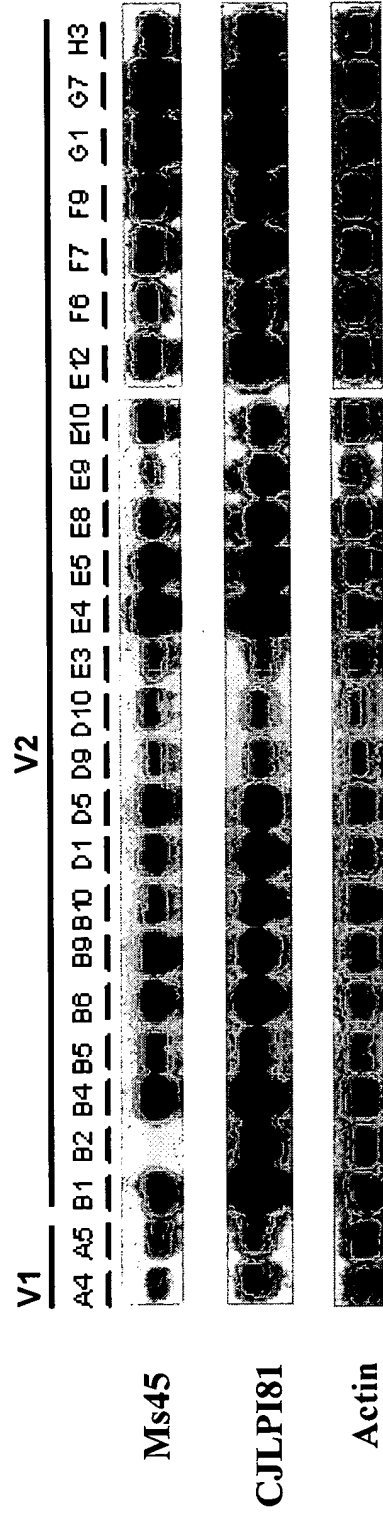


Figure 8

Figure 9

GAP of: Czaal47.Seq check: 446 from: 1 to: 1214
to: Axiglcomplete.Con check: 928 from: 1 to: 3123

Symbol comparison table:
Gencoredisk: [Gcgcore.Data.Rundata]Nwsgapdna.Cmp
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 10871 Length: 3123
Ratio: 8.955 Gaps: 3
Percent Similarity: 100.000 Percent Identity: 100.000

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

Czaal47.Seq x Axiglcomplete.Con May 11, 2000 12:05 ..

```

      . . . . .
1 .....GCAGGAACTTAT 12
      |||||
1101 CGCGTCACTCACGGGTAGCTCATGGTCGAGCGTAGCATGCAGGAACTTAT 1150
      .
13 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 62
      |||||
1151 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 1200
      .
63 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTTCAGCTAGCTAGCTGCG 112
      |||||
1201 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTTCAGCTAGCTAGCTGCG 1250
      .
113 CCGTGACCACGCACATGACCGCAGTGCGCGCGGGGCTGATCAAGGGAAAG 162
      |||||
1251 CCGTGACCACGCACATGACCGCAGTGCGCGCGGGGCTGATCAAGGGAAAG 1300
      .
163 TGATCGGATGGAGCTGGAGCTCGGGCTCGCGCCGCCGAACCCGCATCAGC 212
      |||||
1301 TGATCGGATGGAGCTGGAGCTCGGGCTCGCGCCGCCGAACCCGCATCAGC 1350
      .
213 CGCTGGCTGCCGCCGCCGAGTTCGTCTCGGTCTCCTCAGCAGCTCGGCTGGC 262
      |||||
1351 CGCTGGCTGCCGCCGCCGAGTTCGTCTCGGTCTCCTCAGCAGCTCGGCTGGC 1400
      .
263 TCGTGCGGGAACAAGAGGGTTCTCGGCGACGCGTTCGGGGCCGCCAAGGC 312
      |||||
1401 TCGTGCGGGAACAAGAGGGTTCTCGGCGACGCGTTCGGGGCCGCCAAGGC 1450
      .
313 GGCCACGCTTCCGCTCTTCGTCTGCGAGGATGGCGACGGAGGCGGCGGCG 362
      |||||
1451 GGCCACGCTTCCGCTCTTCGTCTGCGAGGATGGCGACGGAGGCGGCGGCG 1500
```


Sequence Name	SEQ ID NO:	ATCC Deposit
Pioneer clone CZAAL47	1	PTA-2426
ZmAxig1 polypeptide	2	
Native ZmAxig1 promoter region	3	
Modified ZmAxig1 promoter region	4	PTA-2427
A632 full-length ZmAxig1, including SEQ ID No. 3	5	PTA-2426 PTA-2427
Primer 1, used for isolation of 5' flanking region	6	
Primer 2, used for isolation of 5' flanking region	7	
Primer 3, used for isolation of region spanning start codon	8	
Primer 4, used for isolation of region spanning start codon	9	
Primer 5, used for isolation of 5' region	10	
Oligonucleotide designed to remove clones having a poly-A tail but no cDNA	11	
Pioneer clone Cjlp181	12	
CuraGen fragment w0h051.7	13	
Primer 6, used to isolate the coding sequence and 3' region	14	
Primer 7, used to isolate the coding sequence and 3' region	15	
Modified ZmAxig1 promoter region with single-base deletion	16	PTA-2427
LEC1 transcriptional activator element	17	
LEC1 polynucleotides	18-20	
LEC1 polypeptide consensus sequence	21	

Figure 10. Representative polynucleotides and polypeptides of the present invention.

Experiment	Control	Ubi:LEC1	Axig1:LEC1
#1 3938.37	15%	63%	44%
#2 3938.79	4%	17%	20%
#3 3938.78	16%	17%	38%
#4 3938.34	2%	14%	13%

Figure 11. Transformation frequencies by LEC1 with two different promoters. Transformation frequencies were based on the percentage of plated embryos with one or more GFP positive/Bialaphos resistant colonies. All embryos were shot with Ubi:moPAT~GFP (a construct conferring Bialaphos resistance and GFP fluorescence) along with a LEC1 construct or a control DNA.